1645

RAW SEQUENCE LISTING   DATE: 02/13/2002
PATENT APPLICATION: US/09/841,963A   TIME: 15:16:37

Input Set : A:\10545-015.txt
Output Set: N:\CRF3\02132002\I841963A.raw

Does Not Comply
Corrected Diskette Needed

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 3 <110> APPLICANT: Watson, Dennis K.
 4         Papas, Takis S. (Deceased)
 5         Papas, Tula C. (Legal Representative)
 7 <120> TITLE OF INVENTION: Methods and compositions for the diagnosis and treatment of
cancer
 8         based on transcription factor ETS2
10 <130> FILE REFERENCE: 10545-015-999
12 <140> CURRENT APPLICATION NUMBER: 09/841,963A
13 <141> CURRENT FILING DATE: 2001-04-25
15 <150> PRIOR APPLICATION NUMBER: PCT/US99/27805
16 <151> PRIOR FILING DATE: 1999-11-23
18 <150> PRIOR APPLICATION NUMBER: 06/109,850   <- please edit
19 <151> PRIOR FILING DATE: 1998-11-25
21 <160> NUMBER OF SEQ ID NOS: 6
23 <170> SOFTWARE: PatentIn version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1894
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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37 ccagcaggca gccctgggct gggggtaggg gactccctac aggcacgcag ccctgagacc     180
38 gccaccagcc accccttgag ggtggccagg cccccagtgg ccaacctgag tgctgcctct     240
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40 cagtggcctc agctgcccac acctcttccc ggcccctgga gttggcactg cagcagacag     360
41 ctccctgggc accaggcagc taacagacac agccgccagc ccaaacagca gcggc atg      418
42                                                              Met
43                                                               1
44 ggc agc gcc agc ccg ggt ctg agc agc gta tcc ccc agc cac ctc ctg      466
45 Gly Ser Ala Ser Pro Gly Leu Ser Ser Val Ser Pro Ser His Leu Leu
46             5                  10                  15
47 ctg ccc ccc gac acg gtg tcg cgg aca ggc ttg gag aag gcg gca gcg      514
48 Leu Pro Pro Asp Thr Val Ser Arg Thr Gly Leu Glu Lys Ala Ala Ala
49         20                  25                  30
50 ggg gca gtg ggt ctc gag aga cgg gac tgg agt ccc agt cca ccc gcc      562
51 Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro Ala
52     35                  40                  45
53 acg ccc gag cag ggc ctg tcc gcc ttc gac ctc tcc tac ttt gac atg      610
54 Thr Pro Glu Gln Gly Leu Ser Ala Phe Asp Leu Ser Tyr Phe Asp Met
55 50                  55                  60                  65
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56 ctg tac cct gag gac agc agc tgg gca gcc aag gcc cct ggg gcc agc       658
57 Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala Ser
58               70              75              80
59 agt cgg gag gag cca cct gac cag cct gag cag tgc ccg gtc att gac       706
60 Ser Arg Glu Glu Pro Pro Asp Gln Pro Glu Gln Cys Pro Val Ile Asp
61           85              90              95
62 agc caa gcc cca gcg ggc acc ctg gac ttg gtg ccc ggc ggg ctg acc       754
63 Ser Gln Ala Pro Ala Gly Thr Leu Asp Leu Val Pro Gly Gly Leu Thr
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65 ttg gag gag cac tcg ctg gag cag gtg cag tcc atg gtg gtg ggc gaa       802
66 Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly Glu
67       115             120             125
68 gtg ctc aag gac atc gag acg gcc tgc aag ctg ctc aac atc acc gca       850
69 Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr Ala
70 130             135             140             145
71 gat ccc atg gac tgg agc ccc agc aat gtg cag aag tgg ctc ctg tgg       898
72 Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu Trp
73               150             155             160
74 aca gag cac caa tac cgg ctg ccc ccc atg ggc aag gcc ttc cag gag       946
75 Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln Glu
76           165             170             175
77 ctg gcg ggc aag gag ctg tgc gcc atg tcg gag gag cag ttc cgc cag       994
78 Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg Gln
79           180             185             190
80 cgc tcg ccc ctg ggt ggg gat gtg ctg cac gcc cac ctg gac atc tgg      1042
81 Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile Trp
82       195             200             205
83 aag tca gcg gcc tgg atg aaa gag cgg act tca cct ggg gcg att cac      1090
84 Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile His
85 210             215             220             225
86 tac tgt gcc tcg acc agt gag gag agc tgg acc gac agc gag gtg gac      1138
87 Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val Asp
88               230             235             240
89 tca tca tgc tcc ggg cag ccc atc cac ctg tgg cag ttc ctc aag gag      1186
90 Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys Glu
91           245             250             255
92 ttg cta ctc aag ccc cac agc tat ggc cgc ttc att agg tgg ctc aac      1234
93 Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu Asn
94           260             265             270
95 aag gag aag ggc atc ttc aaa att gag gac tca gcc cag gtg gcc cgg      1282
96 Lys Glu Lys Gly Ile Phe Lys Ile Glu Asp Ser Ala Gln Val Ala Arg
97       275             280             285
98 ctg tgg ggc atc cgc aag aac cgt ccc gcc atg aac tgc gac aag ctg      1330
99 Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Cys Asp Lys Leu
100 290            295             300             305
101 agc cgc tcc atc cgc cag tct tac aag aag ggc atc atc cgg aag cca      1378
102 Ser Arg Ser Ile Arg Gln Ser Tyr Lys Lys Gly Ile Ile Arg Lys Pro
103              310             315             320
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108 agccaggccc tgagatgggg gaaaacgggc agtgtgctct gctgctctga ccttccagag   1543
109 cccaaggtca gggaggggca accaactgcc ccagggggat atgggtcctc tggggccttc   1603
110 gggaccatgg ggcaggggtg cttcctcctc aggcccagct gctcccctgg aggacagagg   1663
111 gagacagggc tgctccccaa cacctgcctc tgaccccagc atttccagag cagagcctac   1723
112 agaagggcag tgactcgaca aaggccacag gcagtccagg cctctctctg ctccatcccc   1783
113 ctgcctccca ttctgcacca cacctggcat ggtgcaggga gacatctgca cccctcagtt   1843
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126             20              25              30
128 Ala Gly Ala Val Gly Leu Glu Arg Arg Asp Trp Ser Pro Ser Pro Pro
129         35              40              45
131 Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Asp Leu Ser Tyr Phe Asp
132     50              55              60
134 Met Leu Tyr Pro Glu Asp Ser Ser Trp Ala Ala Lys Ala Pro Gly Ala
135 65              70              75              80
137 Ser Ser Arg Glu Glu Pro Pro Asp Gln Pro Glu Gln Cys Pro Val Ile
138             85              90              95
140 Asp Ser Gln Ala Pro Ala Gly Thr Leu Asp Leu Val Pro Gly Gly Leu
141             100             105             110
143 Thr Leu Glu Glu His Ser Leu Glu Gln Val Gln Ser Met Val Val Gly
144         115             120             125
146 Glu Val Leu Lys Asp Ile Glu Thr Ala Cys Lys Leu Leu Asn Ile Thr
147     130             135             140
149 Ala Asp Pro Met Asp Trp Ser Pro Ser Asn Val Gln Lys Trp Leu Leu
150 145             150             155             160
152 Trp Thr Glu His Gln Tyr Arg Leu Pro Pro Met Gly Lys Ala Phe Gln
153             165             170             175
155 Glu Leu Ala Gly Lys Glu Leu Cys Ala Met Ser Glu Glu Gln Phe Arg
156             180             185             190
158 Gln Arg Ser Pro Leu Gly Gly Asp Val Leu His Ala His Leu Asp Ile
159         195             200             205
161 Trp Lys Ser Ala Ala Trp Met Lys Glu Arg Thr Ser Pro Gly Ala Ile
162     210             215             220
164 His Tyr Cys Ala Ser Thr Ser Glu Glu Ser Trp Thr Asp Ser Glu Val
165 225             230             235             240
167 Asp Ser Ser Cys Ser Gly Gln Pro Ile His Leu Trp Gln Phe Leu Lys
168             245             250             255
170 Glu Leu Leu Leu Lys Pro His Ser Tyr Gly Arg Phe Ile Arg Trp Leu
171             260             265             270
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174         275             280             285
176 Arg Leu Trp Gly Ile Arg Lys Asn Arg Pro Ala Met Asn Cys Asp Lys
177         290             295             300
179 Leu Ser Arg Ser Ile Arg Gln Ser Tyr Lys Lys Gly Ile Ile Arg Lys
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197 tagacctgca ggcctgaggc ctcagactca cactcaaggg gcaagaggcc ctggtggccc  180
198 acctaagagc cacctctgtc cccagccctg ctgccccact gatgtctgac tgagacccag  240
199 cagtgaccct gagctgcctg cccactgcct cctcctggtc cctgaggttg gctctgccga  300
200 ggacggacga ctcttctgaa gcaggcggct aacggaagca gccccaagcc tccaccgcag  360
201 c atg ggc agt gcc agc cca ggc ctg agc aac gtg tcc ccc ggt tgc ctg  409
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207 tca gga gca atg ggc cct gag aag cag gaa tgg agt cct agt cca ccc  505
208 Ser Gly Ala Met Gly Pro Glu Lys Gln Glu Trp Ser Pro Ser Pro Pro
209         35              40              45
210 gcc acc cct gag cag ggc ctg tct gct ttc tac ctc tct tac ttt aac  553
211 Ala Thr Pro Glu Gln Gly Leu Ser Ala Phe Tyr Leu Ser Tyr Phe Asn
212     50              55              60
213 atg tat ccc gac gat agc agc tgg gtc gcc aaa gtc ccc gag gcc cgt  601
214 Met Tyr Pro Asp Asp Ser Ser Trp Val Ala Lys Val Pro Glu Ala Arg
215 65              70              75              80
216 gcc ggg gag gac cac ccg gag gag ccc gag cag tgt ccc gtc att gac  649
217 Ala Gly Glu Asp His Pro Glu Glu Pro Glu Gln Cys Pro Val Ile Asp
218                 85              90              95
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220 Ser Gln Ala Ser Gly Ser Thr Leu Asp Glu His Ser Leu Glu Gln Val
221             100             105             110
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223 Gln Ser Met Val Val Gly Glu Val Leu Lys Asp Ile Glu Thr Ala Cys
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225 aag ctt gtg aac atc aca gca gac cct ggg gac tgg agc cct ggt aac  793
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228 gtg cag aag tgg ctt tta tgg aca gaa cac cag tac cgg ctg cct cca    841
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232 Ala Gly Lys Ala Phe Gln Glu Leu Gly Gly Lys Glu Leu Cys Ala Met
233                 165                 170                 175
234 tcc gag gaa cag ttc cgt cag cgt gca ccc ttg ggt ggg gat gta ctg    937
235 Ser Glu Glu Gln Phe Arg Gln Arg Ala Pro Leu Gly Gly Asp Val Leu
236                 180                 185                 190
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240 acc tcg cct ggg acc ctt cac tac tgc gcc tcc acc agc gag gac ggc    1033
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244 Trp Thr Asp Gly Glu Val Asp Ser Ser Cys Ser Gly Gln Pro Ile His
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246 ctg tgg cag ttc ctg aaa gaa ctg ctg ctc aag ccc cac agc tat ggc    1129
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248                 245                 250                 255
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259 Lys Gly Met Ile Arg Lys Pro Ala Ile Ser Gln Arg Leu Val Tyr Gln
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272 <211> LENGTH: 325
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